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SUPPLEMENTARY INFORMATION

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Sphingolipid biosynthesis modulates plasmodesmal ultrastructure and phloem unloading

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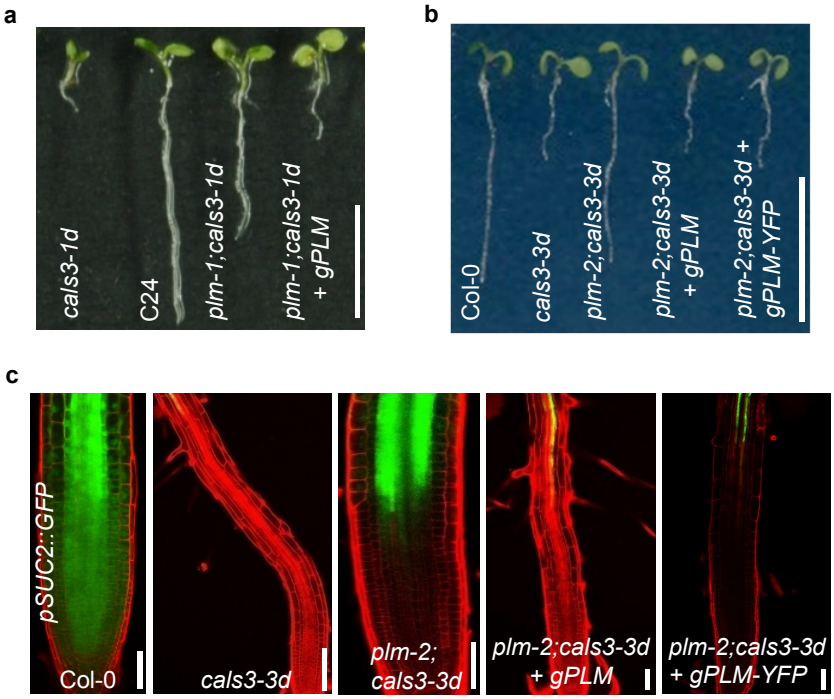
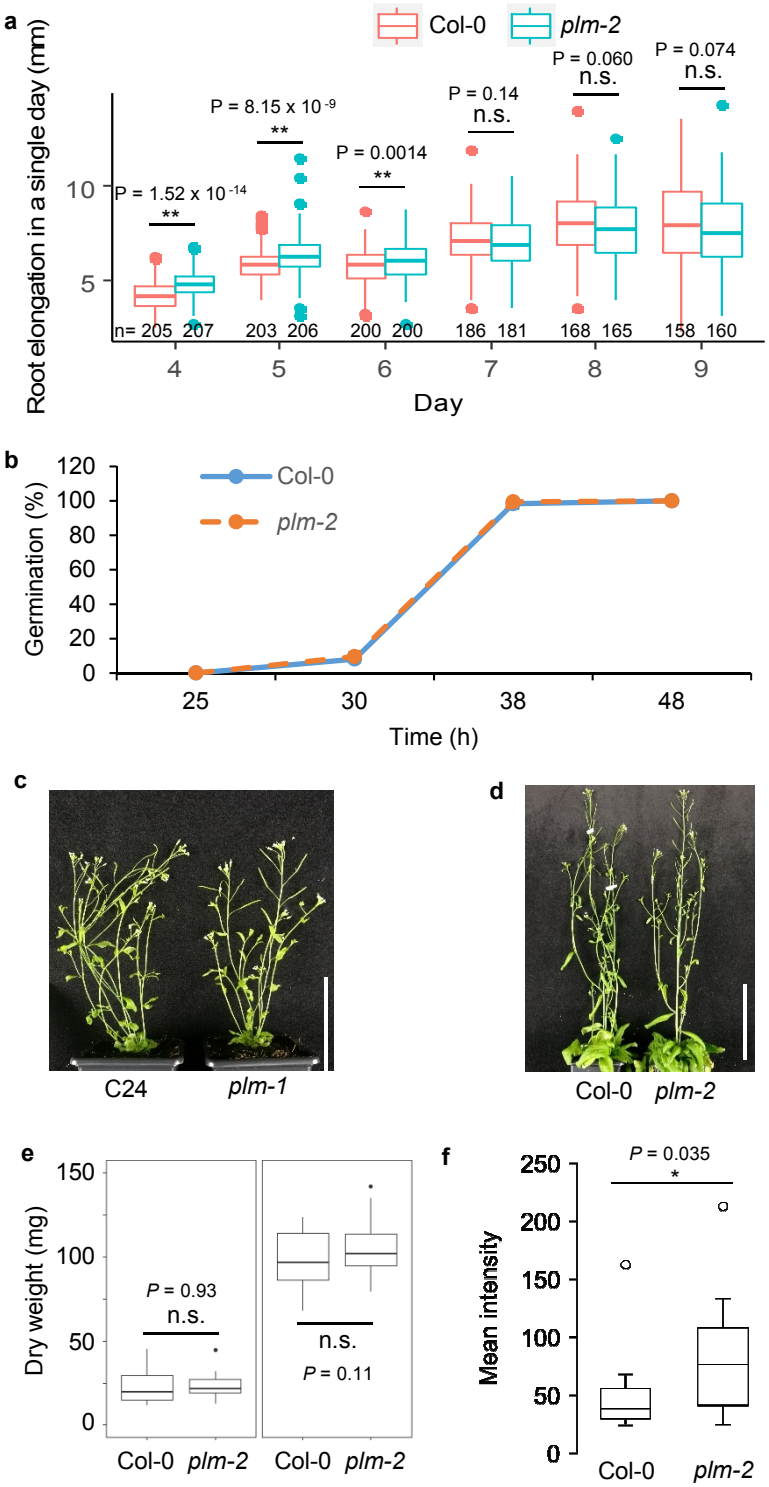
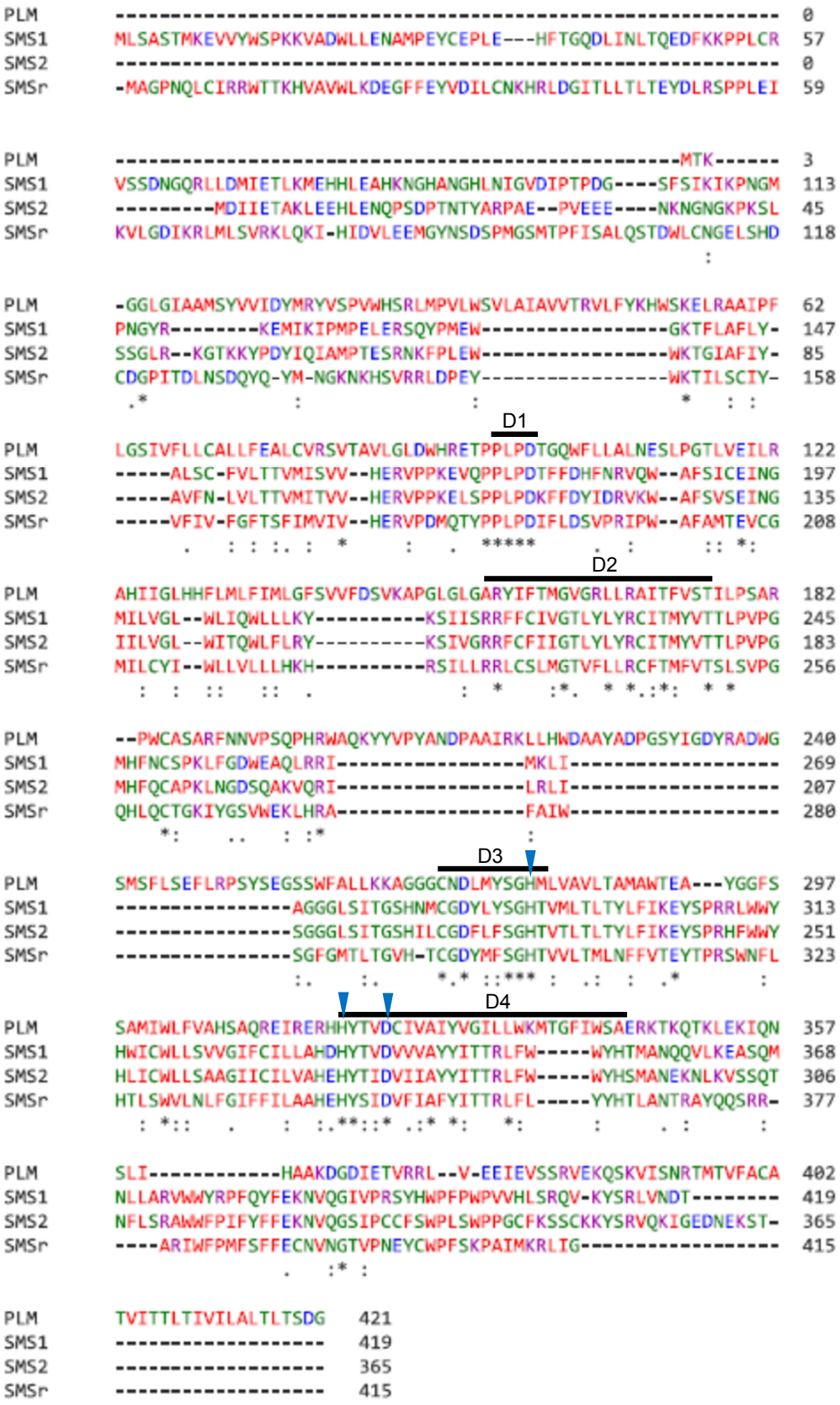
*e-mail: emmanuelle.bayer@u-bordeaux.fr; yrjo.helariutta@slcu.cam.ac.uk



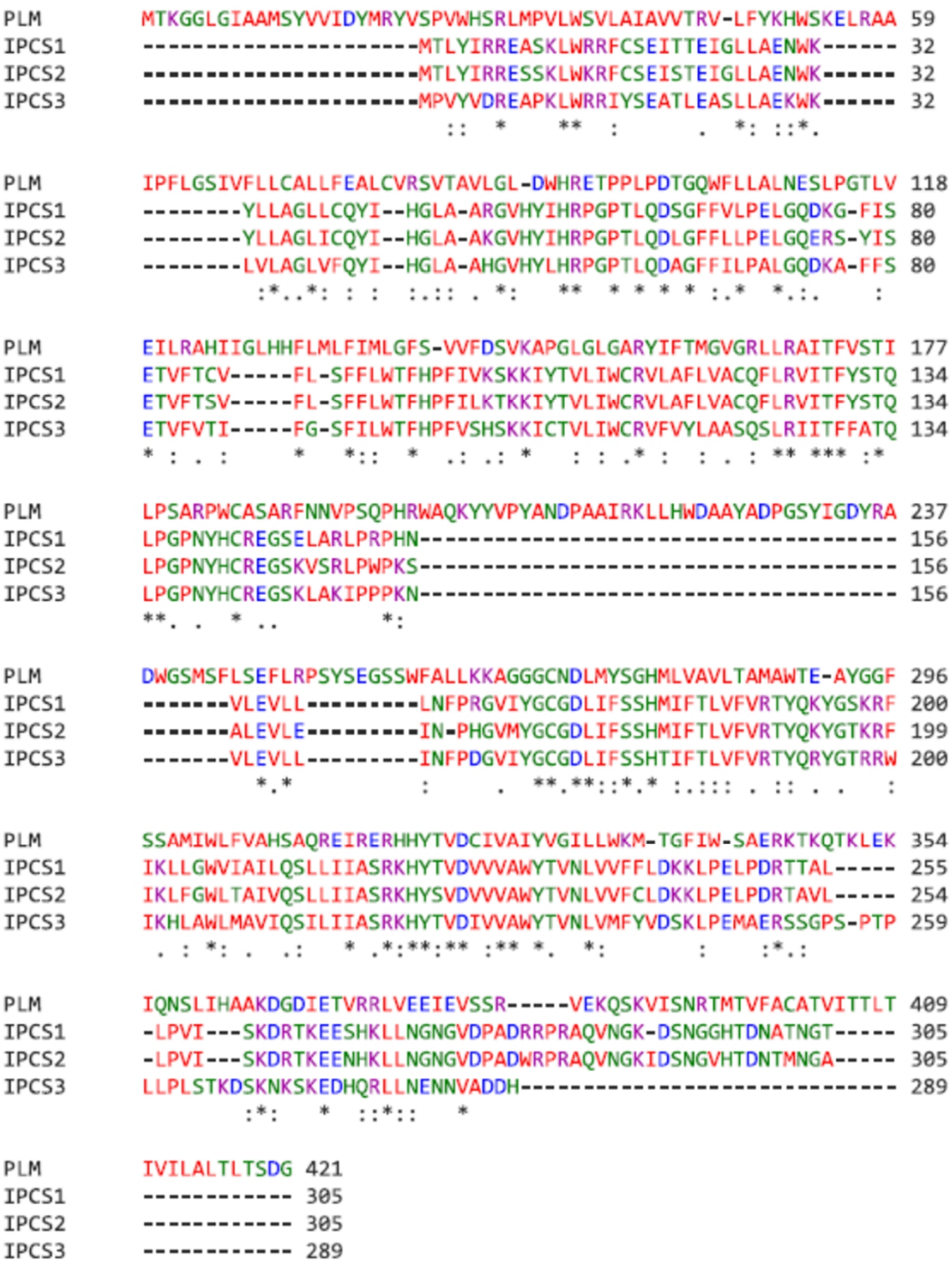
Supplementary Fig. 1. *plm-2* rescues *cals3-3d* in Col-0 background, as well as *plm-1* in C24 background. a. Seedling phenotype of wild-type C24, *cals3-1d*, *plm-1;cals3-1d* and *plm-1;cals3-1d* transformed with PLM genomic insert. The experiment was repeated independently three times with similar results.**b**. Seedling phenotype of wild-type Col-0, *cals3-3d*, *plm-2;cals3-3d* and *plm-2;cals3-2d* transformed with *PLM* genomic and YFP-fusion inserts. **c**. *pSUC2::GFP* in the roots of wild-type Col-0, *cals3-3d*, *plm-2;cals3-3d* and *plm-2;cals3-2d* transformed with *PLM* genomic and YFP-fusion inserts. All the experiments were repeated independently three times with similar results. Scale bars, 1 cm (a, b), 50 μm (c).



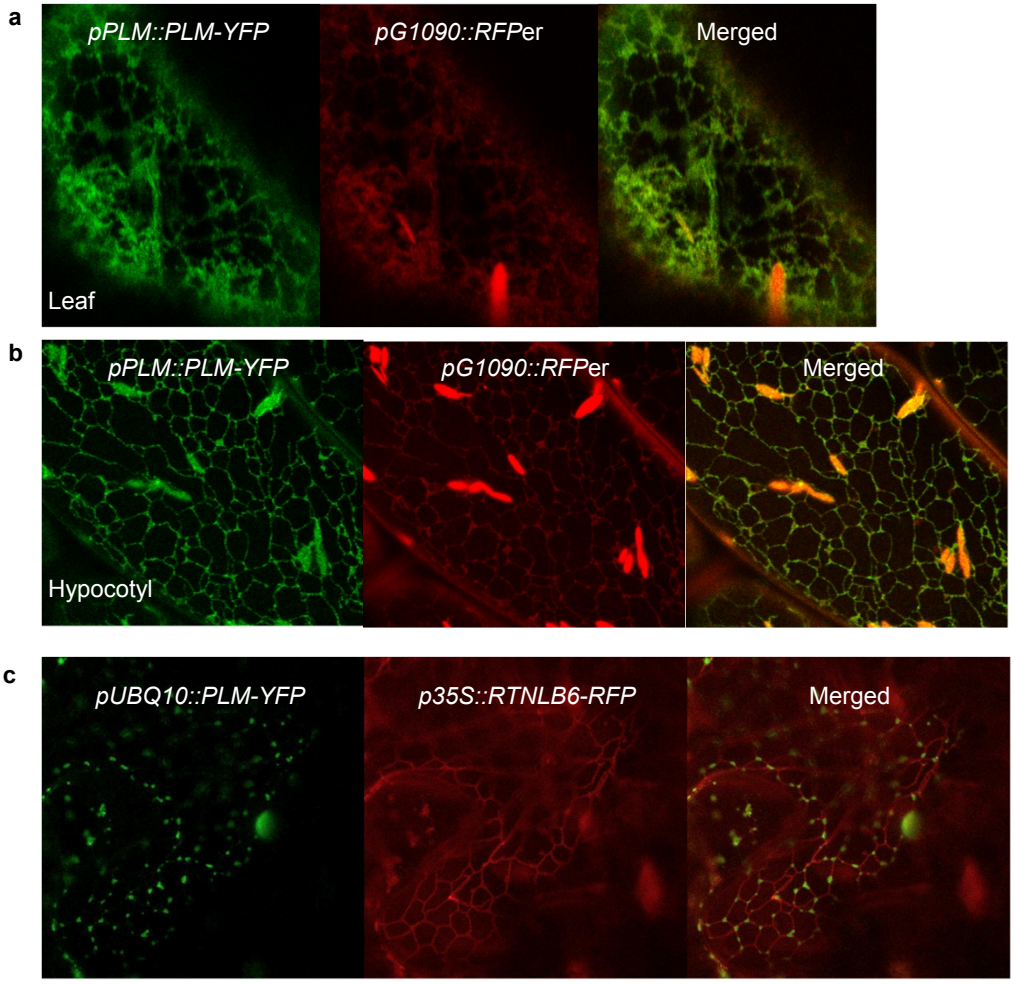
Supplementary Fig. 2. Root elongation and plant biomass assays. a. Root elongation in every single day of Col-0 and *plm-2*. The numbers of biologically independent plants are indicated in the graph. **b.** Germination rate of Col-0 and *plm-2* seeds. Data are based on 3 independent biological replicates with total160 seeds. **c**. Adult plants of C24 and *plm-1*. This experiment was repeated independently three times with similar results. The linear model was use for test. **d**. Adult plants of Col-0 and *plm-2*. This experiment was repeated independently three times with similar results. **e.** Root (left panel) and shoot (right panel) biomass of adult plants at terminal flowering stage. n = 29 (both Col-0 and *plm-2*) biologically independent plants. **f.** GFP intensity in the root tip of 3-day-old seedlings. n = 14 (Col-0), n = 13 (*plm-2*) biologically independent plants. In the box plots, the boxes indicate the first and third quartiles and the whiskers indicate the minimum and maximum values. The black lines within the boxes indicate the median values. Outliers are shown as dots. Significant differences were determined by two-tailed Mann-Whitney-Wilcoxon test. ** *P*<0.01. n.s., no significance.



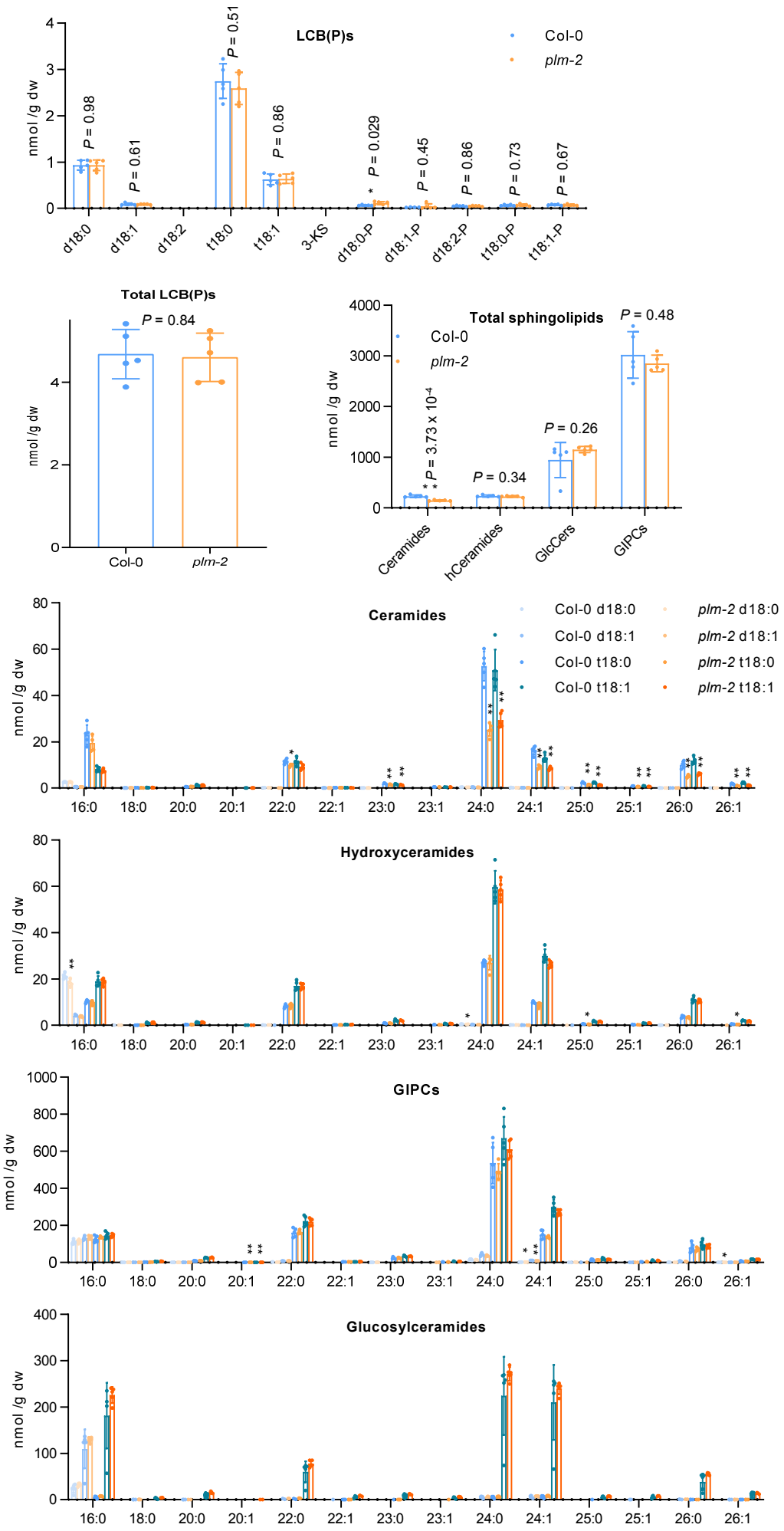
Supplementary Fig. 3. Protein Sequence alignment of PLM (At1g43580) and HsSMSs. Four conserved domains (D1, D2, D3 and D4) within human SMSs are highlighted with black lines. H-H-D residues that form a catalytic triad are highlighted by blue arrows. * , identical residues. ·, similar residues.



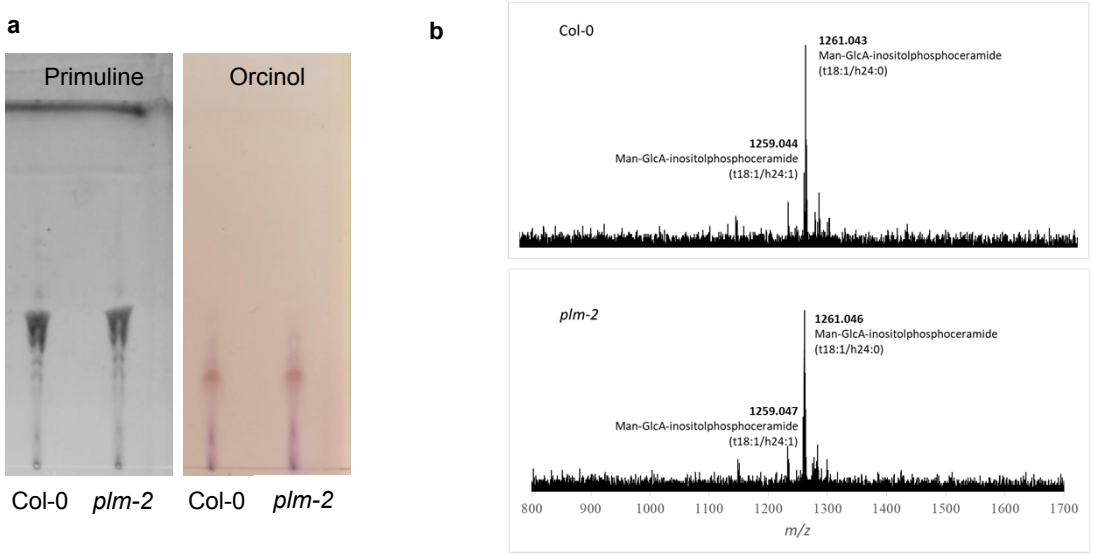
Supplementary Fig. 4. Protein Sequence alignment of PLM (At1g43580) and AtIPCSs. * identical residues. · similar residues.



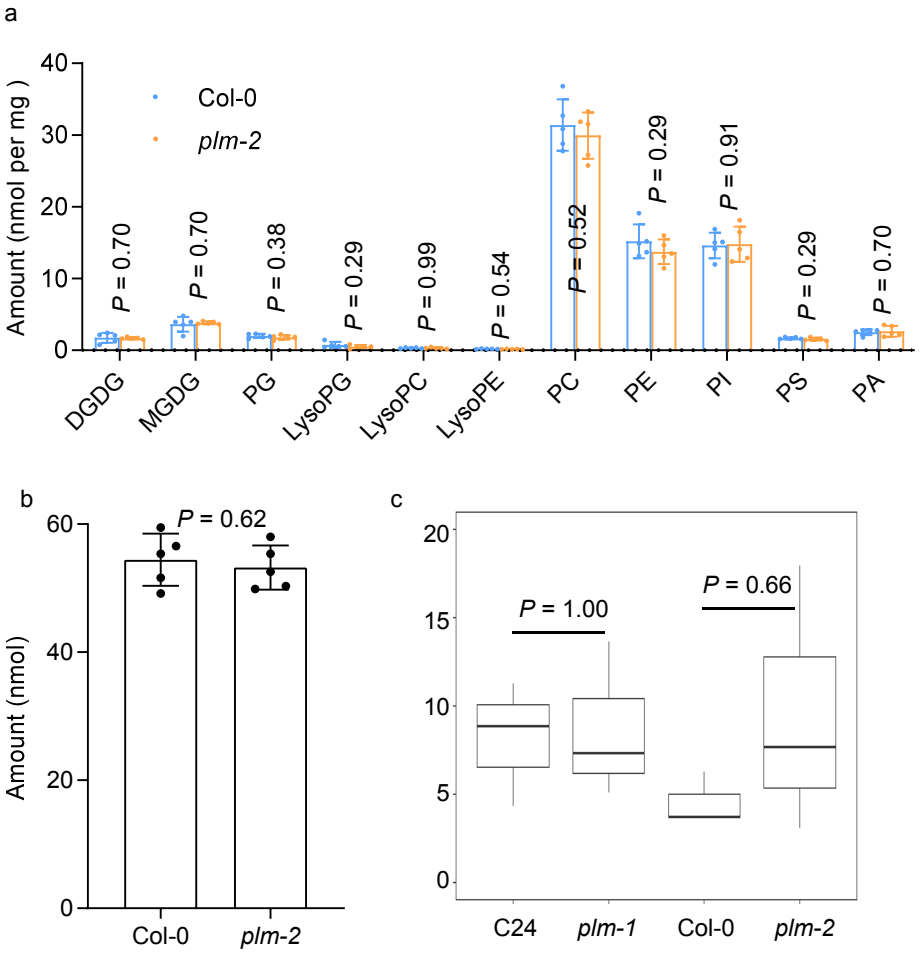
Supplementary Fig 5. Subcellular localization of PLM-YFP. **a**. Co-localization of PLM-YFP with RFPer (RFP-HDEL) in leaf epidermal cells. **b**. Co-localization of PLM-YFP with RFPer in hypocotyl epidermal cells. **c**. Transient co-expression of PLM-YFP with RTNLB6-RFP in the leaf cells of *Nicotiana benthamiana*. All the experiments were repeated independently three times with similar results.



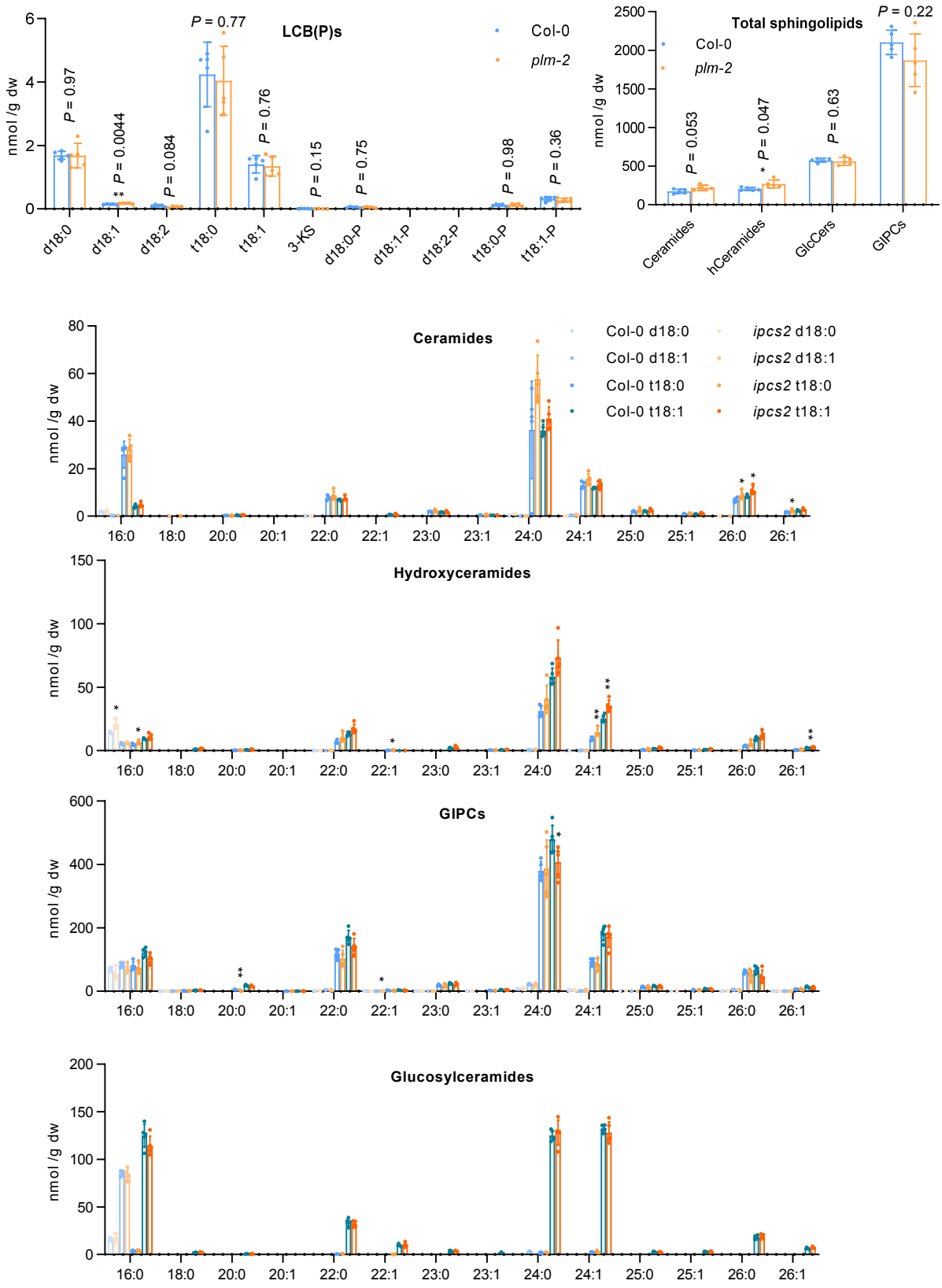
Supplementary Fig.6. Repetition of LCB(P)s and complex sphingolipid species analysis in wild-type Col-0 and *plm-2*. Measurements are the average of five replicates (n = 5 independent samples). Data are means ± SD. Statistically significant differences are indicated by two-tailed Student's t-test. *, *P* <0.05. ** *P* <0.01. hCeramides, hydroxyceramides. GlcCers, glucosylceramides.



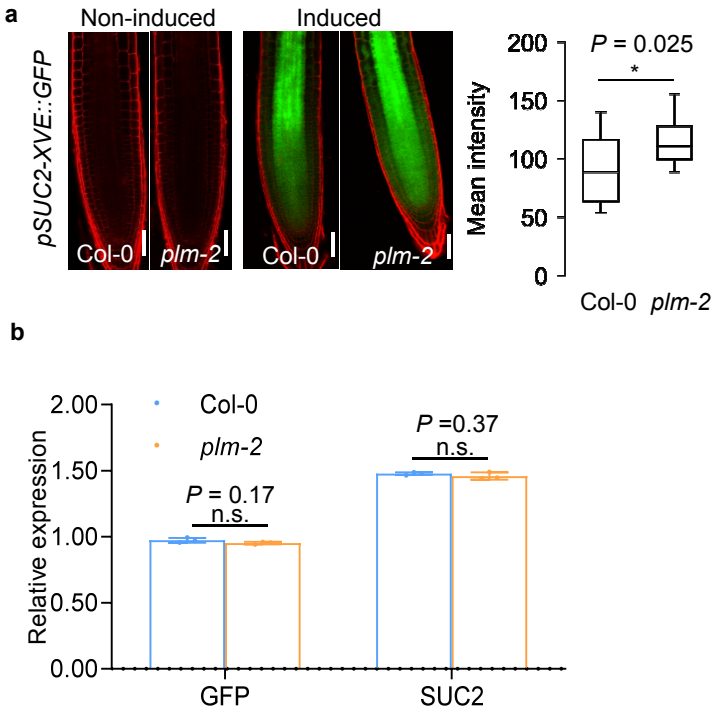
Supplementary Fig. 7. GIPC glycosylation assay. a. Thin layer chromatography (TLC) of an enriched GIPC fraction from 5-day-old roots stained with primuline (binding to certain lipid classes) and orcinol (revealing sugars). **b**. Matrix-assisted laser desorption/ionization mass spectrometry (MALDI-MS) analysis of GIPC enriched fraction from 5-day-old roots to identify highly glycosylated GIPCs. All the experiments were repeated independently two times with similar results.



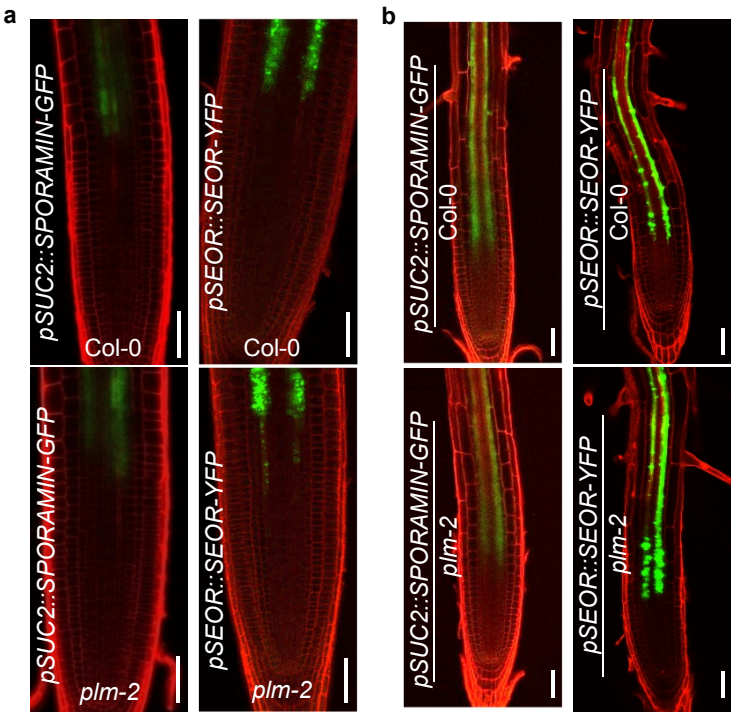
Supplementary Fig. 8. Plant routine lipids profile. a. Plant polar lipids assay in wild-type Col-0 and *plm-2.* Data are means ± SD and based on five replicates (n = 5 independent samples). **b**. Relative amount of DAG in wild-type Col-0 and *plm-2.* Data are means ± SD and based on five replicates with independent samples. **c**. The total sterol amount in 5-day-old seedlings of wild-type and *plm* mutants. Data are based on three replicates with independent samples. The boxes indicate the first and third quartiles and the whiskers indicate the minimum and maximum values. The black lines within the boxes indicate the median values. Significant differences were determined by two-tailed Mann-Whitney-Wilcoxon test. No significances were found between wild type and *plm* mutants in the above assays.



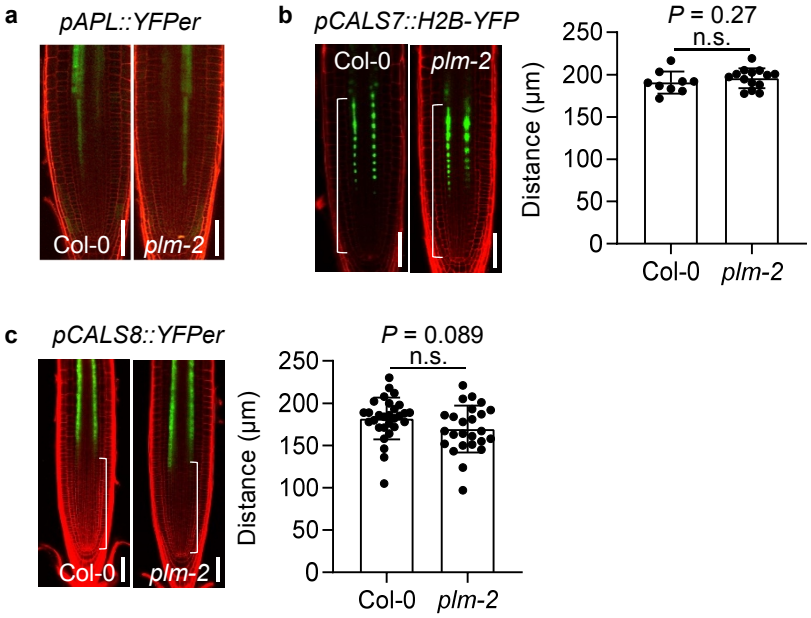
Supplementary Fig.9 Analysis of LCB(P)s and complex sphingolipid species in wild-type Col-0 and *ipcs2* (SALK_206784). Measurements are the average of five replicates (n = 5 independent samples). Data are means ± SD. Statistically significant differences are indicated by two-tailed Student's t-test. *, *P*<0.05. ** *P* <0.01. hCeramides, hydroxyceramides. GlcCers, glucosylceramides.



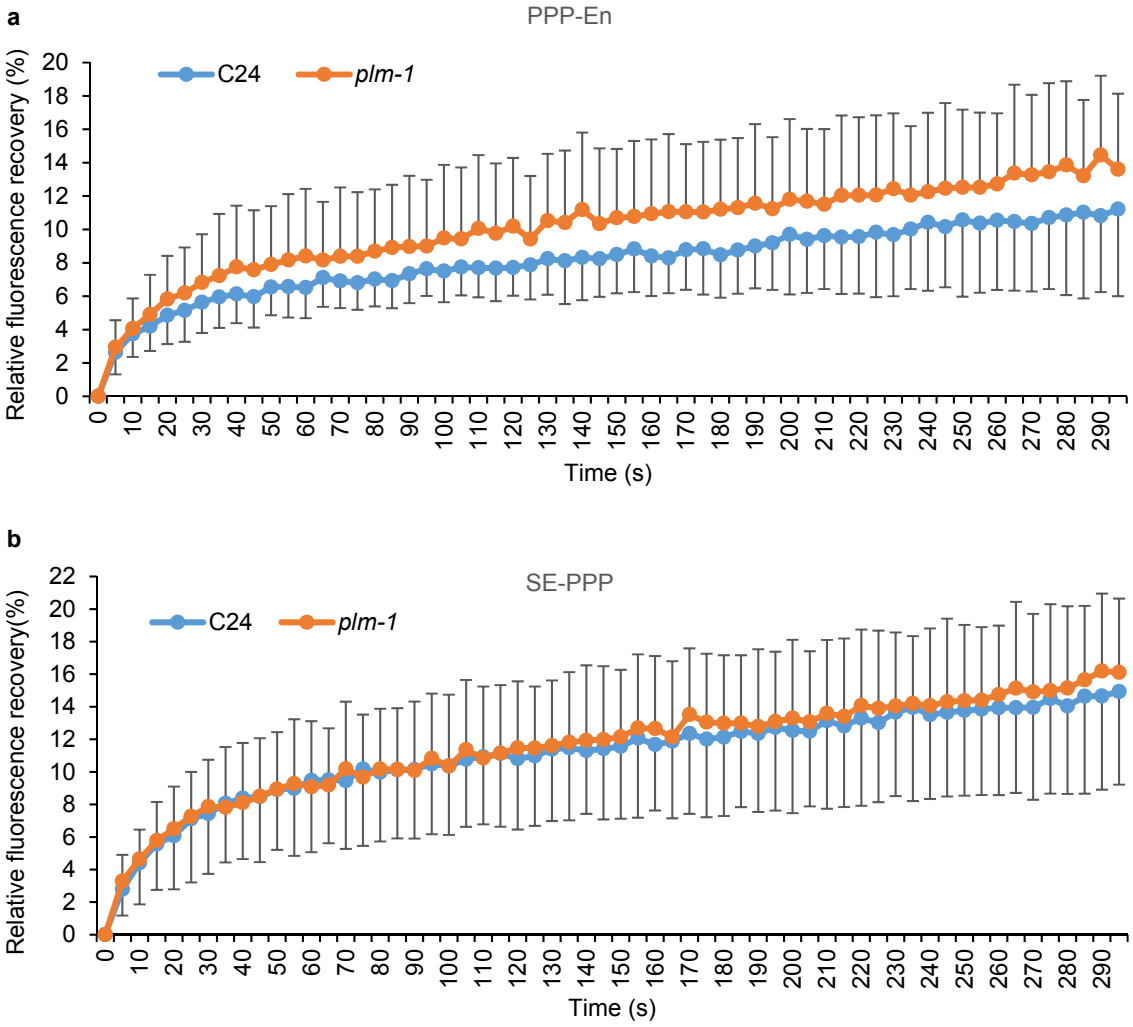
Supplementary Fig.10. *PLM* promotes GFP unloading without affecting *GFP* and *SUC2* expression. a. Col-0 and *plm-2* carrying inducible *pSUC2-XVE::GFP* upon 25h induction by 5 µm β-estradiol. An area of 50 x 40 µm^2 , 50 µm from QC, was used for fluorescence intensity quantification. n = 15 (Col-0), n = 13 (*plm-2)* biologically independent plants. The boxes indicate the first and third quartiles and the whiskers indicate the minimum and maximum values. The black lines within the boxes indicate the median values. **b.** qRT-PCR for GFP and SUC2 transcript levels in wild-type Col-0 and *plm-2*. Data are based on three independent experiments. Data are means ± SD. Significant differences were determined by two-tailed Mann-Whitney-Wilcoxon test (a) and two-sided student's *t*-test (b). * P<0.05. n.s., no significance. Scale bars, 50 µm (**a**).



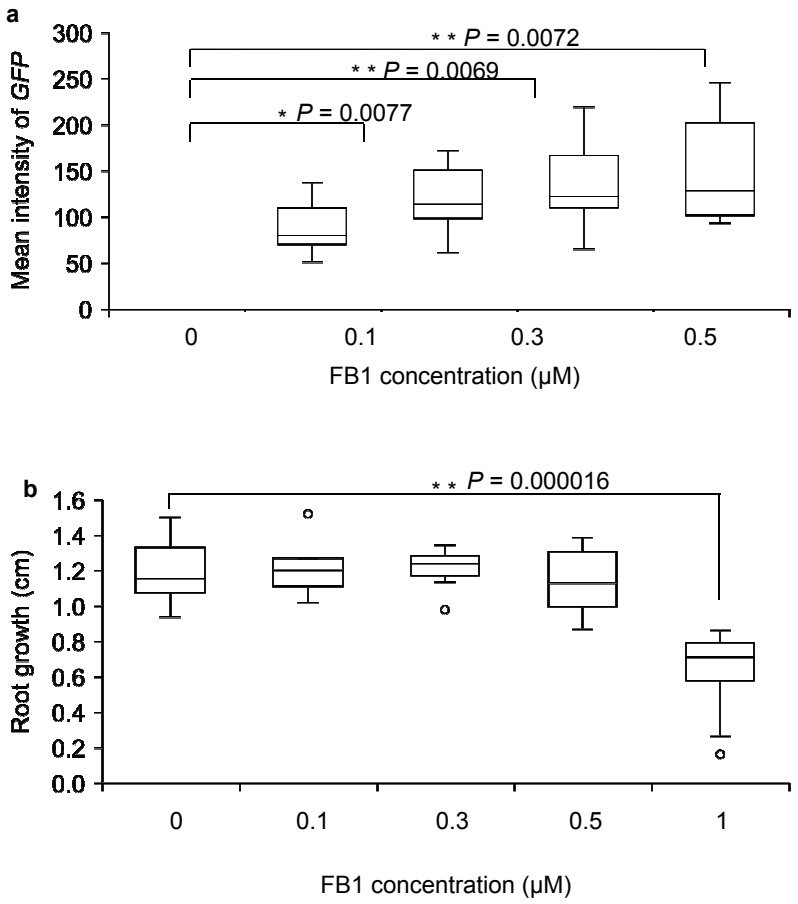
Supplementary Fig. 11. Unloading pattern of GFP fusion proteins with larger size in roots. a. *pSUC2::SPORAMIN-GFP* and *pSEOR::SEOR-YFP* in Col-0 and *plm-2*. **b**. Grafting assay using *pSUC2::SPORAMIN-GFP*[27] and *pSEOR::SEOR-YFP*[26] shoots as scions and Col-0 and *plm-2* roots as stocks. Scale bars, 50 μm (**a**,**b**). the experiment was repeated three times independently with similar results.



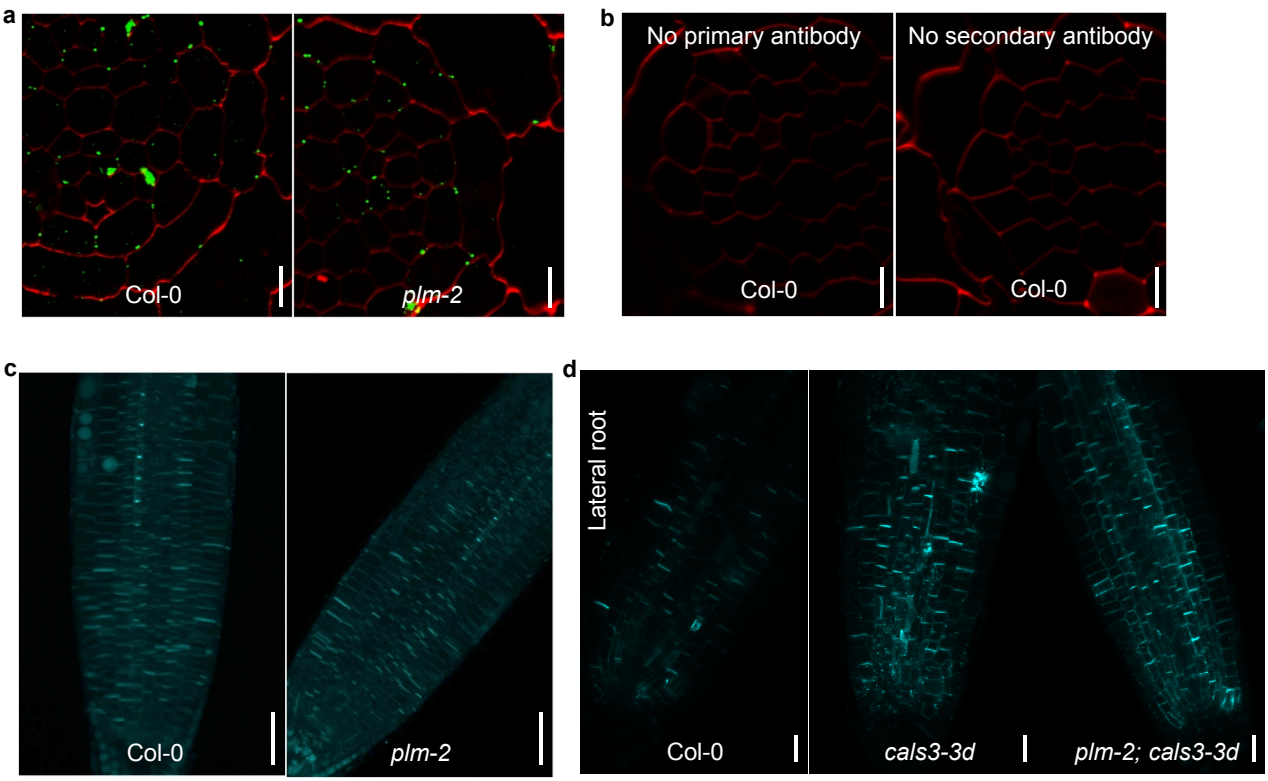
Supplementary Fig. 12. Root phloem development is not impaired by *plm* mutation. a. *pAPL::YFPer* in wild-type Col-0 and *plm-2*. The experiment was repeated four times independently with similar results. **b**. *pCALS7::H2B-YFP*[51] and the distances from QC to the first enucleated cell in wild-type Col-0 (n = 9) and *plm-2* (n = 14) independent plants. **c**. *pCALS8:: YFPer* and the distances from QC to the first expressed cell in wild-type Col-0 (n = 29) and *plm-2* (n = 25) independent plants. Data represent means ± SD. Significant differences were determined by two-tailed student's t test. Scale bars, 50 µm (**a,b,c**).



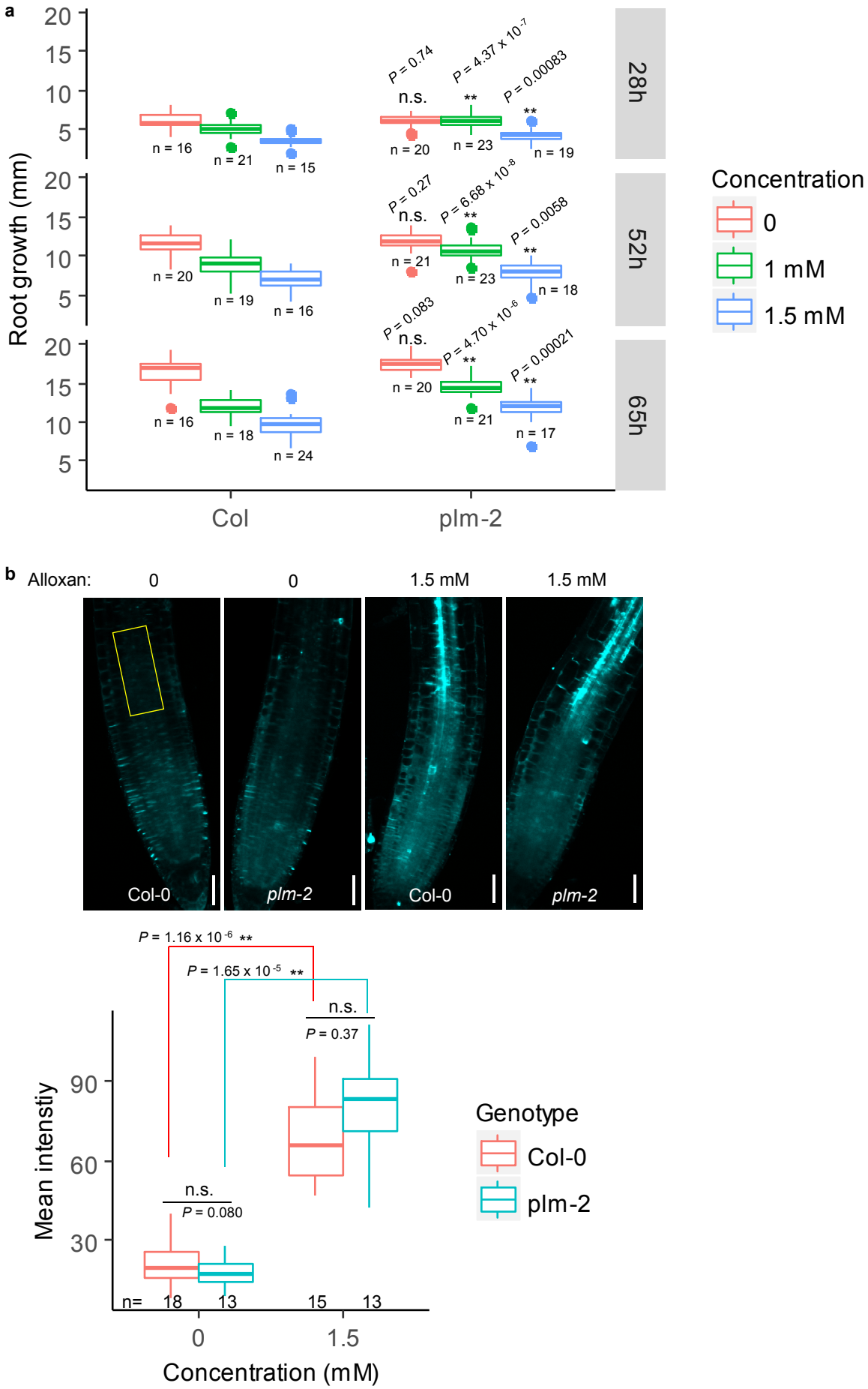
Supplementary Fig 13. FRAP assays in C24 and *plm-1* expressing *pSUC2::GFP*. **a**. GFP movement from PPP to endodermis post bleaching of outward layers in the unloading domain. n= 9 (C24) and 7 (*plm-1*) biologically independent samples. **b**. GFP movement from SE to PPP post bleaching of outward layers in the unloading domain. n= 7 (C24) and 7 (*plm-1*) independent plants. Data represent means ± SD.



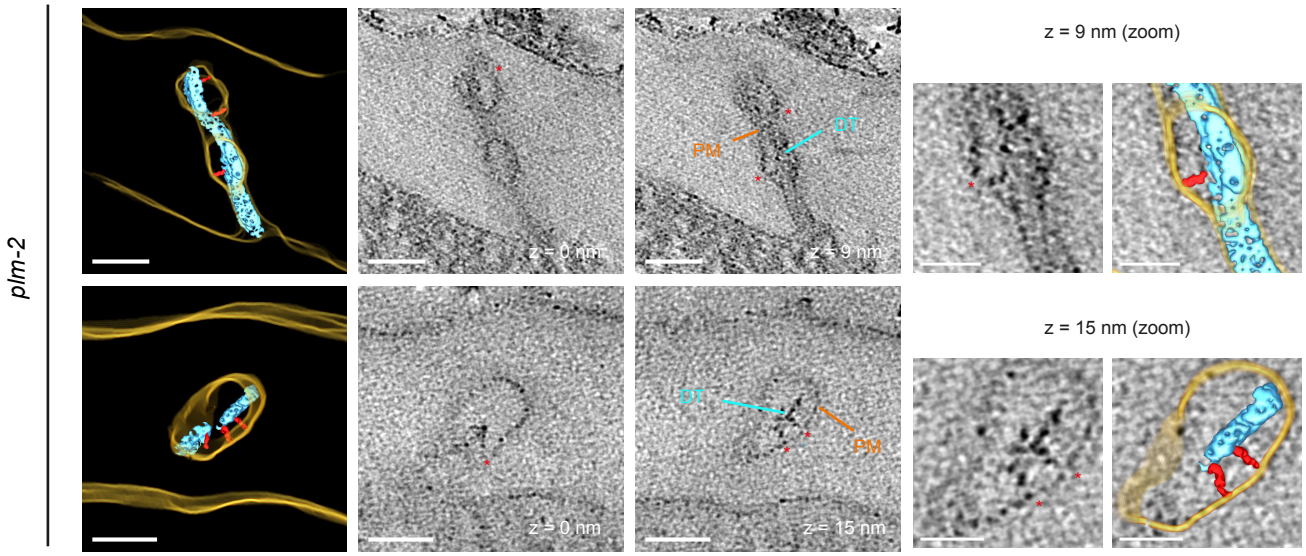
Supplementary Fig. 14. Roots with FBl treatment phenocopies *plm* in enhanced GFP unloading. a. Fluorescence intensity in the root meristem of wild-type Col-0 upon 72h treatment by different concentration of FB1. 3-day-old seedlings growing on normal media were used for treatment. An area of 50 x 40 μm^2, 50 μm from QC, was transferred for quantification. n = 16 (0 μM), n = 14 (0.1 μM), n = 14 (0.3 μM), n = 16 (0.5 μM) independent plants. **b**. Root growth of wild-type Col-0 upon 72h treatment by different concentration of FB1. 3-day-old seedlings growing on normal media were transferred for treatment. n = 10 independent plants for each concentration. The boxes indicate the first and third quartiles and the whiskers indicate the minimum and maximum values. The black lines within the boxes indicate the median values. Outliers are shown as dots. Significant differences were determined by two-tailed Mann-Whitney-Wilcoxon test. *, $P<0.05$. **, $P<0.01$.



Supplementary Fig. 15. Callose deposition analysis. a. Callose deposition (green) in different cell layers shown by immunolocalization using callose antibody. **b**. Immunolocalization controls without primary and secondary antibody. **c**. Aniline blue stained primary roots of wild-type Col-0 and *plm-2*. **d**. Aniline blue stained lateral roots of wild-type Col-0, *cals3-3d* and *cals3-3d;plm-2*. All the experiments were repeated independently three times with similar results. Scale bars, 5 μm (**a**,**b**), 50 μm (**c**,**d**).



Supplementary Fig. 16. Root growth assay by alloxan treatment. 5-day-old seedlings were transferred to same media added with 0, 1, 1.5mM alloxan and the root elongation at 28, 52 and 65h was measured. . **b**. Callose accumulation in roots by aniline blue staining at 28h after transferred to media with 0 and 1.5 mM alloxan. The experiment is repeated three times independently with similar results. A 138 x 60 μm area in the central part starting from transition zone was used for intensity quantification. The boxes indicate the first and third quartiles and the whiskers indicate the minimum and maximum values. The black lines within the boxes indicate the median values. Outliers are shown as dots. Independent plant numbers (n) are indicated in the graphs. Significant differences between Col-0 and *plm-2* under same conditions were determined by two-tailed Mann-Whitney-Wilcoxon test. ** P<0.01. ** P<0.01. n.s., no significance. Scale bars, 50 μm (**b**).



Supplementary Fig. 17. *plm-2* still possesses type II plasmodesmata at the SE-PPP interface of the unloading zone.

Examples of type II plasmodesmata in *plm-2* roots detected with electron tomography at the SE-PPP interface, within the unloading domain. Due to the large size of these PDs the full volume was not contained within the section. Reconstructions are therefore partial with missing volumes. Plasmodesmata are not classified by morphology due to missing volumes that would make the calls arbitrary. In general, they were branched in nature. Panels with black background are 3D reconstructions based on 2D image stacks. Plasma membrane (PM) is rendered in yellow, desmotubule (DT) and ER in light blue, tethers within plasmodesmata in red. Selected 2D views are displayed in the neighbouring panels with zooms for tethers within type II plasmodesmata (with a model overlay). Distance to the first 2D view is indicated under or above each panel. Arrows, symbols and labels indicate various plasmodesmata components and follow the colour scheme of the 3D models (* tether elements within plasmodesmata). Scale bars are of 50nm or 25nm for the zoomed images. Experiment was repeated two times independently with similar results.

Supplementary Table 1. Primer used in this study.

Primer name	Sequence	Used for
MN1.5-F	TTATTATCAAGATCAAAGATTGTATGGTTT	Linked markers for mapping
MN1.5-R	CTTGTTTTTATATCTGTTTGGTTTAATTGT	
CIW12-F	AGGTTTTATTGCTTTTCACA	
CIW12-R	CTTTCAAAAGCACATCACA	
NGA280-F	GGCTCCATAAAAAGTGCACC	
NGA280-R	CTGATCTCACGGACAATAGTGC	
cals3-1d-inner-F	CATAGATTGGATCCTACCTCCAGTGGCAA	Mutation genotyping
cals3-1d-inner-R	AGTGCAGTCTTAAACTGCCGAACACATC	
cals3-1d-outer-F	GCAGCGGCGGATTATACGAACTCA G	
cals3-1d-outer-R	CCCTGCCCATCAGTGTTGGATCATGTT	
cals3-3d-inner-F	GTTGCAGAAAAGACACAGTTGTATGTACT	Mutation genotyping
cals3-3d-inner-R	AGGATCGAGAGGTAGGATATTATCGG	
cals3-3d-outer-F	ATGCTGCTGATAAGGCTGACC	
cals3-3d-outer-R	AGAGCAAGAACAGCAGCTTGG	
plm-2-F	TCTGAAGGGTCTTCTTGGTTTGC	Genotyping
plm-2-R	TTTAGCCGTCGCTTGTCAAAGT	
LBb1.3	ATTTTGCCGATTTCGGAAC	
PLM-m-F	CGGGACACTTGTGGAAATCC	RT-PCR
PLM-m-R	AGTCAATGCCAGAATCACTA	
PLM-p-attB4	GGGGACAACTTTGTATAGAAAAGTTGTGAGTTTTACTTTATACTTCTAAC	*PLM* promoter
PLM-p-attB1r	GGGGACTGCTTTTTTGTACAAACTTGGAAGTGGGTTTAATTAAGCTAA	
PLM-g-attB1	GGGGACAAGTTTGTACAAAAAAGCAGGCTCCATGACTAAAGGTGGACTTGG	*PLM* genomic sequence
PLM-g-attB2	GGGGACCACTTTGTACAAGAAAGCTGGGTCGCCGTCGCTTGTCAAAGTCA	
iSUC2-F	GGGGTACCCCTTGCGGTGGTTGTAGTGGTGGAG	Inducible *SUC2* promoter
iSUC2-R	CCCTCGAGCCACTTTGTTTTGTGGGAGAC	
SUC2-m-F	GCAGACGGGTGAGTTAGA	qPCR
SUC2-m-R	GGAGATTGGACCACAGAG	
GFP-m-F	AAGCTGACCCTGAAGTTCATCTGC	qPCR
GFP-m-R	CTTGTAGTTGCCGTCGTCCTTGAA	

F, forward. R, reversed.

Supplementary Table 2. Protein sequences for phylogenetic tree in Figure.2b.

>Q86VZ5 SMS1_Homo sapiens
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VLKEASQMNLLARVWWYRPFQYFEKNVQGIVPRSYHWPFPWPVVHLSRQVKYSRLVNDT
>Q8NHU3 SMS2_Homo sapiens
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Supplementary Table 3. P values (t-test) of sphingolipid profile analysis. n.d.,no data.

Fig. 3c. C24 and *plm-1* .

Ceramides	16:0	18:0	20:0	20:1	22:0	22:1	23:0	23:1	24:0	24:1	25:0	25:1	26:0	26:1
d18:0	6.85E-01	n.d.	n.d.	n.d.	3.95E-02	n.d.	n.d.	n.d.	1.39E-01	4.00E-03	1.48E-01	n.d.	3.60E-02	n.d.
d18:1	8.57E-01	7.06E-01	n.d.	n.d.	n.d.	7.22E-01	n.d.	n.d.	1.30E-02	4.60E-01	n.d.	n.d.	n.d.	n.d.
t18:0	9.81E-01	7.67E-01	3.71E-01	n.d.	3.00E-02	8.74E-01	5.71E-02	8.07E-01	2.04E-03	5.34E-04	3.90E-02	1.34E-02	1.26E-03	2.42E-04
t18:1	3.19E-01	5.84E-01	1.07E-01	n.d.	8.76E-04	4.45E-01	1.27E-02	8.24E-01	7.10E-05	2.23E-05	3.06E-03	6.84E-03	1.58E-03	2.74E-04

Hydroxyceramides	16:0	18:0	20:0	20:1	22:0	22:1	23:0	23:1	24:0	24:1	25:0	25:1	26:0	26:1
d18:0	1.55E-01	n.d.	n.d.	n.d.	6.68E-01	n.d.	n.d.	n.d.	9.83E-01	3.23E-01	n.d.	n.d.	1.56E-01	n.d.
d18:1	3.49E-03	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	1.74E-01	4.53E-01	n.d.	n.d.	n.d.	n.d.
t18:0	8.51E-01	9.27E-01	4.20E-01	n.d.	8.02E-01	1.51E-01	3.94E-01	5.66E-01	6.60E-01	7.63E-01	9.17E-01	2.46E-01	8.79E-01	5.29E-01
t18:1	2.01E-01	2.54E-01	6.89E-01	n.d.	5.79E-02	2.61E-03	6.24E-02	1.95E-02	5.01E-02	1.36E-01	1.62E-02	1.43E-01	5.87E-02	2.49E-01

GIPCs	16:0	18:0	20:0	20:1	22:0	22:1	23:0	23:1	24:0	24:1	25:0	25:1	26:0	26:1
d18:0	8.75E-01	2.11E-01	1.62E-01	n.d.	6.45E-01	n.d.	2.45E-01	n.d.	9.35E-01	9.73E-01	n.d.	n.d.	5.83E-01	7.48E-01
d18:1	2.35E-02	6.49E-01	9.04E-01	n.d.	4.45E-02	n.d.	n.d.	n.d.	1.91E-02	8.27E-04	4.65E-01	9.64E-01	2.58E-01	2.44E-01
t18:0	6.54E-01	8.69E-02	1.62E-01	1.03E-01	9.24E-01	9.77E-01	4.47E-01	3.25E-01	7.74E-01	5.25E-01	7.46E-01	3.92E-01	6.87E-01	9.61E-01
t18:1	2.27E-02	3.22E-01	1.31E-01	1.40E-02	1.22E-02	1.21E-02	5.82E-02	4.37E-02	2.67E-02	9.07E-02	1.95E-01	4.53E-02	2.94E-01	2.52E-01

Glucosylceramides	16:0	18:0	20:0	20:1	22:0	22:1	23:0	23:1	24:0	24:1	25:0	25:1	26:0	26:1
d18:0	6.65E-01	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
d18:1	3.11E-03	3.72E-01	6.55E-01	n.d.	6.09E-02	n.d.	n.d.	n.d.	3.38E-02	9.85E-02	n.d.	n.d.	2.17E-01	7.43E-02
t18:0	7.24E-01	n.d.	n.d.	n.d.	5.21E-01	n.d.	5.63E-01	n.d.	6.45E-01	2.50E-01	n.d.	n.d.	7.45E-01	8.14E-01
t18:1	1.34E-02	5.85E-01	6.77E-02	n.d.	2.32E-02	3.69E-03	5.07E-02	1.35E-02	1.04E-02	1.88E-03	1.66E-01	2.10E-02	1.08E-01	3.63E-01

Fig. 3d. Col-0 and *plm-2* .

Ceramides	16:0	18:0	20:0	20:1	22:0	22:1	23:0	23:1	24:0	24:1	25:0	25:1	26:0	26:1
d18:0	2.51E-01	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
d18:1	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	1.21E-01	n.d.	n.d.	n.d.	n.d.
t18:0	5.37E-01	n.d.	1.15E-01	n.d.	6.58E-02	n.d.	2.67E-03	1.92E-01	1.46E-04	2.90E-04	8.37E-03	9.70E-03	1.70E-04	2.89E-04
t18:1	4.70E-01	n.d.	7.22E-01	n.d.	7.71E-03	3.78E-02	1.30E-04	2.49E-02	4.09E-06	9.32E-07	3.80E-04	6.07E-03	3.50E-06	5.44E-05

Hydroxyceramides	16:0	18:0	20:0	20:1	22:0	22:1	23:0	23:1	24:0	24:1	25:0	25:1	26:0	26:1
d18:0	7.16E-01	n.d.	n.d.	n.d.	7.74E-03	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
d18:1	5.06E-01	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	9.58E-01	6.32E-01	n.d.	n.d.	n.d.	n.d.
t18:0	1.96E-01	n.d.	1.87E-01	n.d.	4.28E-02	5.20E-02	n.d.	6.50E-01	9.37E-02	5.72E-02	9.04E-02	3.59E-01	1.36E-01	8.40E-01
t18:1	1.48E-02	4.16E-03	1.18E-02	n.d.	2.08E-02	n.d.	5.38E-02	1.73E-02	3.51E-02	1.28E-02	6.29E-02	2.89E-02	4.51E-02	1.02E-01

GIPCs	16:0	18:0	20:0	20:1	22:0	22:1	23:0	23:1	24:0	24:1	25:0	25:1	26:0	26:1
d18:0	9.69E-02	2.65E-01	n.d.	n.d.	1.01E-02	n.d.	6.78E-01	8.72E-01	3.32E-03	4.89E-03	n.d.	n.d.	5.82E-01	4.73E-02
d18:1	3.07E-01	5.53E-01	n.d.	n.d.	5.70E-02	1.30E-01	n.d.	n.d.	3.27E-03	9.70E-01	n.d.	n.d.	2.73E-04	7.80E-04
t18:0	7.12E-02	2.38E-02	1.86E-02	9.72E-02	1.97E-02	1.77E-02	9.30E-03	3.87E-02	2.31E-03	1.92E-03	5.05E-03	2.86E-02	3.18E-05	2.00E-04
t18:1	2.82E-02	3.53E-02	8.86E-02	2.18E-01	3.08E-02	5.16E-01	1.08E-02	4.99E-02	3.81E-03	8.59E-03	7.30E-04	1.66E-03	3.21E-02	2.29E-03

Glucosylceramides	16:0	18:0	20:0	20:1	22:0	22:1	23:0	23:1	24:0	24:1	25:0	25:1	26:0	26:1
d18:0	6.39E-01	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
d18:1	2.83E-01	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
t18:0	1.32E-01	n.d.	n.d.	n.d.	5.78E-03	n.d.	n.d.	n.d.	3.48E-01	4.98E-01	n.d.	n.d.	n.d.	n.d.
t18:1	7.62E-01	4.63E-02	2.41E-02	n.d.	2.80E-01	7.20E-04	6.96E-02	n.d.	2.20E-02	2.42E-01	5.02E-01	1.37E-01	6.03E-02	8.71E-01

Fig. S6. Col-0 and *plm-2* .

Ceramides	16:0	18:0	20:0	20:1	22:0	22:1	23:0	23:1	24:0	24:1	25:0	25:1	26:0	26:1
d18:0	5.91E-01	n.d.	n.d.	n.d.	1.94E-01	n.d.	7.58E-01	n.d.	5.16E-01	5.78E-01	5.53E-01	n.d.	5.17E-01	n.d.
d18:1	1.17E-01	5.27E-01	n.d.	n.d.	n.d.	6.33E-01	n.d.	n.d.	1.09E-01	3.69E-02	n.d.	n.d.	1.36E-01	n.d.
t18:0	1.67E-01	2.15E-01	6.72E-01	n.d.	2.17E-02	7.71E-01	3.15E-03	1.22E-01	1.95E-04	3.64E-04	5.97E-04	1.30E-04	9.20E-04	1.18E-04
t18:1	2.66E-01	1.23E-01	2.47E-01	6.99E-01	6.61E-02	3.23E-01	1.33E-03	9.20E-01	3.59E-03	1.60E-03	4.24E-04	8.44E-04	4.71E-04	2.55E-04

Hydroxyceramides	16:0	18:0	20:0	20:1	22:0	22:1	23:0	23:1	24:0	24:1	25:0	25:1	26:0	26:1
d18:0	6.28E-03	n.d.	n.d.	n.d.	7.41E-01	n.d.	n.d.	n.d.	9.48E-01	4.55E-02	n.d.	n.d.	7.33E-01	n.d.
d18:1	6.15E-02	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	7.22E-01	3.87E-01	n.d.	n.d.	n.d.	n.d.
t18:0	5.43E-01	7.73E-02	1.96E-01	n.d.	6.39E-01	4.61E-01	5.56E-01	5.94E-01	8.85E-01	5.04E-02	4.35E-02	9.40E-02	3.47E-01	3.82E-02
t18:1	9.08E-01	5.81E-01	8.41E-01	6.90E-01	9.33E-01	7.39E-01	6.17E-01	6.82E-01	7.91E-01	5.20E-02	7.21E-01	3.17E-01	3.89E-01	9.67E-02

GIPCs	16:0	18:0	20:0	20:1	22:0	22:1	23:0	23:1	24:0	24:1	25:0	25:1	26:0	26:1
d18:0	5.25E-01	1.15E-01	3.81E-01	n.d.	4.34E-01	n.d.	3.90E-01	n.d.	2.43E-01	3.19E-02	5.51E-01	n.d.	3.04E-01	4.23E-02
d18:1	5.73E-01	4.09E-01	5.00E-01	n.d.	9.25E-01	n.d.	n.d.	n.d.	6.21E-02	5.14E-03	n.d.	2.70E-01	2.52E-01	1.37E-01
t18:0	3.69E-01	6.62E-01	6.25E-01	4.71E-03	8.98E-01	7.09E-01	8.14E-01	9.42E-01	4.53E-01	3.62E-01	7.21E-01	8.13E-01	4.39E-01	7.12E-01
t18:1	8.46E-01	8.75E-02	2.05E-01	5.41E-03	8.21E-01	1.32E-01	5.58E-01	1.25E-01	3.30E-01	1.66E-01	3.11E-01	2.38E-01	3.36E-01	2.13E-01

Glucosylceramides	16:0	18:0	20:0	20:1	22:0	22:1	23:0	23:1	24:0	24:1	25:0	25:1	26:0	26:1

d18:0	1.07E-01	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
d18:1	3.50E-01	6.41E-01	9.60E-01	n.d.	1.38E-01	n.d.	n.d.	n.d.	3.10E-01	4.54E-01	n.d.	n.d.	2.68E-01	7.09E-02
t18:0	7.04E-02	n.d.	n.d.	n.d.	9.46E-02	8.38E-02	n.d.	n.d.	2.28E-01	1.84E-01	n.d.	n.d.	2.05E-01	9.67E-01
t18:1	2.36E-01	2.24E-01	7.28E-02	n.d.	1.63E-01	1.03E-01	1.69E-01	1.46E-01	2.80E-01	4.53E-01	2.99E-01	2.23E-01	1.01E-01	5.01E-01

Fig. S9. Col-0 and *ipcs2* .

Ceramides	16:0	18:0	20:0	20:1	22:0	22:1	23:0	23:1	24:0	24:1	25:0	25:1	26:0	26:1
d18:0	6.79E-01	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
d18:1	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	8.72E-02	n.d.	n.d.	n.d.	n.d.
t18:0	5.04E-01	n.d.	7.60E-01	n.d.	3.23E-01	n.d.	2.98E-01	4.57E-01	8.15E-02	8.61E-02	4.10E-01	9.42E-01	4.94E-02	4.90E-02
t18:1	2.72E-01	n.d.	2.08E-01	n.d.	3.08E-01	2.33E-01	9.32E-01	9.28E-01	9.43E-02	9.94E-02	1.41E-01	6.44E-02	2.21E-02	9.31E-02

Hydroxyceramides	16:0	18:0	20:0	20:1	22:0	22:1	23:0	23:1	24:0	24:1	25:0	25:1	26:0	26:1
d18:0	1.35E-02	n.d.	n.d.	n.d.	5.32E-02	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
d18:1	2.03E-01	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	4.45E-01	7.86E-01	n.d.	n.d.	n.d.	n.d.
t18:0	4.97E-02	n.d.	1.52E-01	n.d.	9.47E-02	2.09E-02	n.d.	6.02E-01	1.28E-01	9.81E-03	2.07E-01	3.64E-01	1.29E-01	6.22E-02
t18:1	1.26E-01	6.88E-02	1.40E-01	n.d.	6.28E-02	n.d.	1.53E-01	6.51E-02	7.90E-02	3.67E-03	6.06E-02	5.36E-02	1.21E-01	3.42E-03

GIPCs	16:0	18:0	20:0	20:1	22:0	22:1	23:0	23:1	24:0	24:1	25:0	25:1	26:0	26:1
d18:0	1.10E-01	9.71E-02	n.d.	n.d.	2.99E-01	2.33E-01	9.33E-01	1.76E-01	9.88E-01	5.75E-01	n.d.	n.d.	1.69E-01	2.84E-01
d18:1	1.18E-01	7.55E-01	n.d.	n.d.	3.86E-01	1.68E-02	n.d.	n.d.	7.34E-01	6.83E-02	n.d.	n.d.	1.17E-01	2.93E-01
t18:0	3.64E-01	3.89E-01	2.39E-03	4.07E-01	2.91E-01	1.91E-01	4.09E-01	3.39E-01	8.72E-01	1.98E-01	6.37E-01	4.92E-01	2.60E-01	9.52E-01
t18:1	7.66E-02	1.56E-01	1.49E-01	5.82E-01	8.49E-02	1.30E-01	5.64E-01	1.48E-01	4.18E-02	5.26E-01	1.86E-01	1.79E-01	9.61E-02	5.28E-01

Glucosylceramides	16:0	18:0	20:0	20:1	22:0	22:1	23:0	23:1	24:0	24:1	25:0	25:1	26:0	26:1
d18:0	4.48E-01	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
d18:1	4.79E-01	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
t18:0	9.65E-01	n.d.	n.d.	n.d.	8.31E-01	n.d.	n.d.	n.d.	8.05E-01	6.09E-01	n.d.	n.d.	n.d.	n.d.
t18:1	1.70E-01	2.65E-01	2.12E-01	n.d.	4.05E-01	9.00E-01	7.17E-01	n.d.	6.30E-01	4.47E-01	8.33E-01	4.97E-01	4.98E-01	1.66E-01